

SEQUENCE LISTING

<110> Ozelius, Laurie J.
Breakefield, Xandra O.

<120> TORSIN, TORSIN-RELATED GENES, AND
METHODS OF DETECTING NEURONAL DISEASES

<130> 0838.1001009

<150> 09/461,921

<151> 1999-12-15

<150> US 09/218,363

<151> 1998-12-22

<150> US 09/099,454

<151> 1998-06-18

<150> US 60/050,244

<151> 1997-06-19

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<170> FastSEQ for Windows Version 4.0

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aacaaagatg gcggccgccc gcgtcgggag gagggctgcc ctgaagaaag atggcctccg 480
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Met Lys Leu Gly Arg Ala Val Leu Gly
1 5
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ctc tac tgc ctc ttc gcc gag tgc tgc ggg cag aag cgg agc ctt agc	738
Leu Tyr Cys Leu Phe Ala Glu Cys Cys Gly Gln Lys Arg Ser Leu Ser	
45 50 55	
cgg gag gca ctg cag aag gat ctg gac gac aac ctc ttt gga cag cat	786
Arg Glu Ala Leu Gln Lys Asp Leu Asp Asp Asn Leu Phe Gly Gln His	
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ctt gca aag aaa atc atc tta aat gcc gtg ttt ggt ttc ata aac aac	834
Leu Ala Lys Lys Ile Ile Leu Asn Ala Val Phe Gly Phe Ile Asn Asn	
75 80 85	
cca aag ccc aag aaa cct ctc acg ctc tcc ctg cac ggg tgg aca ggc	882
Pro Lys Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp Thr Gly	
90 95 100 105	
acc ggc aaa aat ttc gtc agc aag atc atc gca gag aat att tac gag	930
Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala Glu Asn Ile Tyr Glu	
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ggt ggt ctg aac agt gac tat gtc cac ctg ttt gtg gcc aca ttg cac	978
Gly Gly Leu Asn Ser Asp Tyr Val His Leu Phe Val Ala Thr Leu His	
125 130 135	
ttt cca cat gct tca aac atc acc ttg tac aag gat cag tta cag ttg	1026
Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys Asp Gln Leu Gln Leu	
140 145 150	
tgg att cga ggc aac gtg agt gcc tgt gcg agg tcc atc ttc ata ttt	1074
Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg Ser Ile Phe Ile Phe	
155 160 165	
gat gaa atg gat aag atg cat gca ggc ctc ata gat gcc atc aag cct	1122
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170 175 180 185	
ttc ctc gac tat tat gac ctg gtg gat ggg gtc tcc tac cag aaa gcc	1170
Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val Ser Tyr Gln Lys Ala	
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atg ttc ata ttt ctc agc aat gct gga gca gaa agg atc aca gat gtg	1218
Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu Arg Ile Thr Asp Val	
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gct ttg gat ttc tgg agg agt gga aag cag agg gaa gac atc aag ctc	1266
Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg Glu Asp Ile Lys Leu	
220 225 230	
aaa gac att gaa cac gcg ttg tct gtg tcg gtt ttc aat aac aag aac	1314
Lys Asp Ile Glu His Ala Leu Ser Val Ser Val Phe Asn Asn Lys Asn	
235 240 245	

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agt ggc ttc tgg cac agc agc tta att gac cgg aac ctc att gat tat 1362
 Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg Asn Leu Ile Asp Tyr 265
 250 255 260

ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac cta aaa atg tgt atc 1410
 Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His Leu Lys Met Cys Ile 280
 270 275

cga gtg gaa atg cag tcc cga ggc tat gaa att gat gaa gac att gta 1458
 Arg Val Glu Met Gln Ser Arg Gly Tyr Glu Ile Asp Glu Asp Ile Val 295
 285 290

agc aga gtg gct gag gag atg aca ttt ttc ccc aaa gag gag aga gtt 1506
 Ser Arg Val Ala Glu Glu Met Thr Phe Phe Pro Lys Glu Glu Arg Val 310
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 Phe Ser Asp Lys Gly Cys Lys Thr Val Phe Thr Lys Leu Asp Tyr Tyr 325
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 Tyr Asp Asp 330

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 35 40 45
 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
 50 55 60
 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
 65 70 75 80
 Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
 85 90 95

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Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
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Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
      115      120      125
Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
      130      135      140
Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
      145      150      155      160
Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
      165      170      175
Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
      180      185      190
Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
      195      200      205
Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
      210      215      220
Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
      225      230      235      240
Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
      245      250      255
Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
      260      265      270
Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
      275      280      285
Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
      290      295      300
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taactgcaac ctccgcctcc tgggttcaag agattctcct gcctcaacct ccgagtagct 180
gggattacag gcgyscgccr csmcrsccag cntttttttt tttttttgag acagtttcgc 240
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gttcaagaga ttctnctgcc tcaactcccg agtagctggg attataggng nccgcnacca 360
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gnccctmacc aaccatggcc gnccnaagg gagtggggcg ggtctgcggg gcggaagtga 780
cgsacgagag gaagtccgtc ctgcgcttgg ccgcggggcg cctggctcag tggcttctgc 840

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gcaggtcggc	catcacccggc	tacctgtcct	aca atg aca tct act gcc cgt tcg			1014
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ccg agt gct gcc ggc gag gag cgg ccg ctc aac gct tcg gct ctc aag						1062
Pro Ser Ala Ala Gly Glu Glu Arg Pro Leu Asn Ala Ser Ala Leu Lys	10	15	20			
ctg gat ttg gag gag aag ctg ttt gga cag cat cta gcc acg gaa gtg						1110
Leu Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val	25	30	35			
att ttc aag gcg ctg act ggc ttc agg aac aac aaa aat ccc aag aaa						1158
Ile Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys	40	45	50			55
cca ctg acc ctt tcc tta cac ggc tgg gct ggc aca ggc aag aat ttt						1206
Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe	60	65	70			
gtc agt caa att gtg gct gaa aat ctt cac cca aaa ggt ctg aag agt						1254
Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser	75	80	85			
aac ttt gtc cac ctg ttt gta tcg act ctg cac ttc cct cat gag cag						1302
Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln	90	95	100			
aag ata aaa ctg tac cag gac cag tta cag aag tgg atc cgc ggt aat						1350
Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn	105	110	115			
gtg agt gca tgt gcg aac tct gtt ttc ata ttt gac gag atg gat aaa						1398
Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys	120	125	130			135
ttg cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac						1446
Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr	140	145	150			
gag cag gtt gac gga gtg tct tac cgc aaa gcc atc ttc atc ttt ctc						1494
Glu Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu	155	160	165			
agc aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg						1542
Ser Asn Ala Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp	170	175	180			
cgg gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct						1590
Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro	185	190	195			
gta ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac						1638
Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His	200	205	210			215

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				25					30					35		

tac atc tac ccg cgt ctc tac tgc ctc ttc gcc gag tgc tgc ggg cag	198
Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu Cys Cys Gly Gln	
40 45 50	
aag cgg agc ctt agc cgg gag gca ctg cag aag gat ctg gac gac aac	246
Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp Leu Asp Asp Asn	
55 60 65	
ctc ttt gga cag cat ctt gca aag aaa atc atc tta aat gcc gtg ttt	294
Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu Asn Ala Val Phe	
70 75 80	
ggg ttc ata aac aac cca aag ccc aag aaa cct ctc acg ctc tcc ctg	342
Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu Thr Leu Ser Leu	
85 90 95 100	
cac ggg tgg aca ggc acc ggc aaa aat ttc gtc agc aag atc atc gca	390
His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala	
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gag aat att tac gag ggt ggt ctg aac agt gac tat gtc cac ctg ttt	438
Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr Val His Leu Phe	
120 125 130	
gtg gcc aca ttg cac ttt cca cat gct tca aac atc acc ttg tac aag	486
Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys	
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Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg	
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tcc atc ttc ata ttt gat gaa atg gat aag atg cat gca ggc ctc ata	582
Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His Ala Gly Leu Ile	
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Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu	
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Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg	
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Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val	
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Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg	
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aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870
Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His	
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Leu	Asp	Asp	Asn	Leu	Phe	Gly	Gln	His	Leu	Ala	Lys	Lys	Ile	Ile	Leu		
65					70					75					80		
Asn	Ala	Val	Phe	Gly	Phe	Ile	Asn	Asn	Pro	Lys	Pro	Lys	Lys	Pro	Leu		
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Thr	Leu	Ser	Leu	His	Gly	Trp	Thr	Gly	Thr	Gly	Lys	Asn	Phe	Val	Ser		
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Lys	Ile	Ile	Ala	Glu	Asn	Ile	Tyr	Glu	Gly	Gly	Leu	Asn	Ser	Asp	Tyr		
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Val	His	Leu	Phe	Val	Ala	Thr	Leu	His	Phe	Pro	His	Ala	Ser	Asn	Ile		
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Thr	Leu	Tyr	Lys	Asp	Gln	Leu	Gln	Leu	Trp	Ile	Arg	Gly	Asn	Val	Ser		
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 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
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 Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
 195 200 205
 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
 210 215 220
 Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 225 230 235 240
 Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255
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 275 280 285
 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
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 Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys Pro
 20 25 30

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 35 40 45

agt caa att gtg gct gaa aat ctt cac cca aaa ggt ctg aag agt aac 193
 Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser Asn
 50 55 60

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 65 70 75 80

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 85 90 95

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 Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys Leu
 100 105 110

cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac gag 385
 His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Glu
 115 120 125

cag gtt gac gga gtg tct tac cgc aaa gcc atc ttc atc ttt ctc agc 433
 Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu Ser
 130 135 140

aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg cgg 481
 Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp Arg
 145 150 155 160

gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct gta 529
 Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val
 165 170 175

ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac agt 577
 Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser
 180 185 190

gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct 625
 Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro
 195 200 205

ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg gcc 673
 Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala
 210 215 220

cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa 721
 Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu
 225 230 235 240

atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc 769
 Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys
 245 250 255

aag act gtg cag tgc cgg ctg gat ttc cac tgagctccta tccagatggg 819
 Lys Thr Val Gln Ser Arg Leu Asp Phe His
 260 265

gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa 879
 gaccgctttg gggttttgccc tgtttgcacc ttagactttt gggatatagaa tctttttttt 939
 gagaagaggt ctactccgt catccaagct ggagtgcagt ggtgcaatcc tcaactcact 999
 gcaacctccg ctcccgttt gagtgattct catgcctcag cctcccagat agctgggatt 1059
 acaggcatga gccactgtgc ccagctggga tatagaatct aagagttgat tgtggaaaac 1119
 acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtcca gctgttcttt 1179
 gcagctggag atgaactttt aaaaatcccc ttcacactta atgtactgac cgagacagaa 1239
 gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcaccgcc 1299
 gcctcagaag ctacggtcac aactaaagga gtccaggggac ttgctgcagg ctgggggggca 1359
 ctgggtgggt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct 1419
 tttgctctgt ctgcgttctt acacagagtt cactgacttg aagtatactc agttaaaatc 1479
 ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgcccgc cgagcactct 1539
 tgatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct 1599
 gcagcagacc tggacagaca ggcccctccc gcctgtccat cgctctagct gctaatacag 1659
 ccctggctgt ggaatccttc accgtctcag ctggtatcag cccagcctg ccttggtgcc 1719
 atatctcagc ttggatctct gctagagtcc cccaacatc atatcataga gttgaatcac 1779

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aatgagaccg ttggctttga atttgagtcg ttgggtccca tgggtgagatg cttgttaaga 1839
ctttatactt ggggtcaatct ctcactttat tttgtagaac catttgaaat cctaggatgt 1899
gcttggtctg gaaggatgac atgggcccag actgaacaag tcagcttgat gatcttaaat 1959
gatggaagta taggacgttg cttattttaa aacaagggaa ggacacaaaa tggaatgact 2019
gccttagtcc tttctcagat actccttaaa acaatttttt attgtttaaa tttgtggtaa 2079
tacatgggtca caaccgtgga tcaaacaagg tcagtctaaa gtggcaggtc ctaggtgtga 2139
cctgatacca ccaccctttg tggcagcacc gggctggact gccctgatcc ctgggacgtg 2199
agacttagct tccagccagt gtgaatcatt gtatctgtct cataatcaca gcacagctgc 2259
agacacaaca acgtgcagca ttttttacat aaaaatatgg tagaattaat ttatgacatg 2319
gaaatgcctt acgtgggtatc acacttagtc ttgaaaaaaa caccaagggtg acgtttaaaa 2379
tttttagtac atatcctcaa attggagcta agttatactt cttttataac cttttgggca 2439
tctggctcag agaagacaag attttctcta tttacagtga ggcaataaat atgtttgcca 2499
cctttt                                     2504

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<210> 8
 <211> 266
 <212> PRT
 <213> Homo sapien

<400> 8

Asp	Leu	Glu	Glu	Lys	Leu	Phe	Gly	Gln	His	Leu	Ala	Thr	Glu	Val	Ile
1				5					10					15	
Phe	Lys	Ala	Leu	Thr	Gly	Phe	Arg	Asn	Asn	Lys	Asn	Pro	Lys	Lys	Pro
			20					25					30		
Leu	Thr	Leu	Ser	Leu	His	Gly	Trp	Ala	Gly	Thr	Gly	Lys	Asn	Phe	Val
		35				40					45				
Ser	Gln	Ile	Val	Ala	Glu	Asn	Leu	His	Pro	Lys	Gly	Leu	Lys	Ser	Asn
	50					55					60				
Phe	Val	His	Leu	Phe	Val	Ser	Thr	Leu	His	Phe	Pro	His	Glu	Gln	Lys
65					70					75					80
Ile	Lys	Leu	Tyr	Gln	Asp	Gln	Leu	Gln	Lys	Trp	Ile	Arg	Gly	Asn	Val
				85				90					95		
Ser	Ala	Cys	Ala	Asn	Ser	Val	Phe	Ile	Phe	Asp	Glu	Met	Asp	Lys	Leu
			100					105					110		
His	Pro	Gly	Ile	Ile	Asp	Ala	Ile	Lys	Pro	Phe	Leu	Asp	Tyr	Tyr	Glu
		115					120					125			
Gln	Val	Asp	Gly	Val	Ser	Tyr	Arg	Lys	Ala	Ile	Phe	Ile	Phe	Leu	Ser
	130					135					140				
Asn	Ala	Gly	Gly	Asp	Leu	Ile	Thr	Lys	Thr	Ala	Leu	Asp	Phe	Trp	Arg
145					150					155					160
Ala	Gly	Arg	Lys	Arg	Glu	Asp	Ile	Gln	Leu	Lys	Asp	Leu	Glu	Pro	Val
				165				170						175	
Leu	Ser	Val	Gly	Val	Phe	Asn	Asn	Lys	His	Ser	Gly	Leu	Trp	His	Ser
			180					185					190		
Gly	Leu	Ile	Asp	Lys	Asn	Leu	Ile	Asp	Tyr	Phe	Ile	Pro	Phe	Leu	Pro
		195					200					205			
Leu	Glu	Tyr	Arg	His	Val	Lys	Met	Cys	Val	Arg	Ala	Glu	Met	Arg	Ala
	210					215					220				
Arg	Gly	Ser	Ala	Ile	Asp	Glu	Asp	Ile	Val	Thr	Arg	Val	Ala	Glu	Glu
225					230					235					240
Met	Thr	Phe	Phe	Pro	Arg	Asp	Glu	Lys	Ile	Tyr	Ser	Asp	Lys	Gly	Cys
				245					250					255	
Lys	Thr	Val	Gln	Ser	Arg	Leu	Asp	Phe	His						
			260					265							

<210> 9
 <211> 332
 <212> PRT
 <213> Homo sapien

<400> 9

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Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Leu Ala Pro Ser
 1          5          10          15
Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
          20          25          30
Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
          35          40          45
Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
          50          55          60
Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
65          70          75          80
Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
          85          90          95
Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
          100          105          110
Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
          115          120          125
Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
          130          135          140
Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
145          150          155          160
Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
          165          170          175
Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
          180          185          190
Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
          195          200          205
Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
          210          215          220
Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
225          230          235          240
Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
          245          250          255
Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
          260          265          270
Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
          275          280          285
Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
          290          295          300
Thr Phe Phe Pro Lys Glu Glu Pro Val Phe Ser Asp Lys Gly Cys Lys
305          310          315          320
Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
          325          330

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<210> 10

<211> 267

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(267)

<223> Xaa = any amino acid

<400> 10

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Leu Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val
 1          5          10          15
Ile Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys
          20          25          30

```

Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe
 35 40 45
 Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser
 50 55 60
 Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln
 65 70 75 80
 Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn
 85 90 95
 Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys
 100 105 110
 Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr
 115 120 125
 Glu Gln Val Asp Gly Val Ser Tyr Xaa Lys Ala Ile Phe Ile Phe Leu
 130 135 140
 Ser Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp
 145 150 155 160
 Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro
 165 170 175
 Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His
 180 185 190
 Ser Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu
 195 200 205
 Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg
 210 215 220
 Ala Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu
 225 230 235 240
 Glu Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gln
 245 250 255
 Cys Lys Thr Val Gln Ser Arg Leu Asp Phe His
 260 265

<210> 11
 <211> 334
 <212> PRT
 <213> C. elegans

<400> 11
 Met Trp Met Lys Leu Asp Tyr Val Leu Leu Leu Leu Phe His Leu Cys
 1 5 10 15
 Phe Val Asn Thr Glu Leu Ile Ser Val Ile Thr Gly Lys Ile Lys Asp
 20 25 30
 Ser Gly Thr Thr Ile Ala Ile Ser Ala Gly Ala Phe Trp Gly Leu Lys
 35 40 45
 Asp Arg Leu Lys Cys Tyr Leu Tyr Glu Cys Cys His Glu Pro Asp Val
 50 55 60
 Asn Phe Asn Tyr His Thr Leu Asp Ala Asp Ile Ala Asn Leu Leu Phe
 65 70 75 80
 Gly Gln His Leu Val Lys Asp Val Val Val Asn Ser Ile Lys Ser His
 85 90 95
 Trp Tyr Asn Glu Asn Pro Arg Lys Pro Leu Val Leu Ser Phe His Gly
 100 105 110
 Tyr Thr Gly Ser Gly Lys Asn Tyr Val Ala Glu Ile Ile Ala Asn Asn
 115 120 125

 Thr Phe Arg Leu Gly Leu Arg Ser Thr Phe Val Gln His Ile Val Ala
 130 135 140
 Thr Asn Asp Phe Pro Asp Lys Asn Lys Leu Glu Glu Tyr Gln Val Glu
 145 150 155 160

Leu Arg Asn Arg Ile Leu Thr Thr Val Gln Lys Cys Gln Arg Ser Ile
 165 170 175
 Phe Ile Phe Asp Glu Ala Asp Lys Leu Pro Glu Gln Leu Leu Gly Ala
 180 185 190
 Ile Lys Pro Phe Leu Asp Tyr Tyr Ser Thr Ile Ser Gly Val Asp Phe
 195 200 205
 Arg Arg Ser Ile Phe Ile Leu Ser Asn Lys Gly Gly Gly Glu Ile
 210 215 220
 Ala Arg Ile Thr Lys Glu Gln Tyr Glu Ser Gly Tyr Pro Arg Glu Gln
 225 230 235 240
 Leu Arg Leu Glu Ala Phe Glu Arg Glu Leu Met Asn Phe Ser Tyr Asn
 245 250 255
 Glu Lys Gly Gly Leu Gln Met Ser Glu Leu Ile Ser Asn His Leu Ile
 260 265 270
 Asp His Phe Val Pro Phe Leu Pro Leu Gln Arg Glu His Val Arg Ser
 275 280 285
 Cys Val Gly Ala Tyr Leu Arg Lys Arg Gly Arg Gly Asp Leu Val Ser
 290 295 300
 Asn Val Asp Phe Val Glu Arg Val Leu Asn Ser Leu Gln Tyr Phe Pro
 305 310 315 320
 Glu Ser Ser Lys Ala Phe Ser Ser Ser Gly Cys Lys Arg Val
 325 330

<210> 12
 <211> 268
 <212> PRT
 <213> Homo sapien

<400> 12
 Leu Glu Cys Asp Leu Ala Gln His Leu Ala Gly Gln His Leu Ala Lys
 1 5 10 15
 Ala Leu Val Val Lys Ser Leu Lys Ala Phe Val Gln Asp Pro Ala Pro
 20 25 30
 Ser Lys Pro Leu Val Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys
 35 40 45
 Ser Tyr Val Ser Ser Leu Leu Ala Gln His Leu Phe Arg Asp Gly Leu
 50 55 60
 Arg Ser Pro His Val His His Phe Ser Pro Ile Ile His Phe Pro His
 65 70 75 80
 Pro Ser Arg Thr Glu Gln Tyr Lys Lys Glu Leu Lys Ser Trp Val Gln
 85 90 95
 Gly Asn Thr Ala Cys Glu Arg Ser Leu Phe Leu Phe Asp Glu Met Asp
 100 105 110
 Lys Leu Pro Pro Gly Leu Met Glu Val Leu Gln Pro Phe Leu Gly Pro
 115 120 125
 Ser Trp Val Val Tyr Gly Thr Asn Tyr Arg Lys Ala Ile Phe Ile Phe
 130 135 140
 Ile Ser Asn Ala Gly Gly Glu Cys Ile Asn Gln Val Ala Leu Glu Ala
 145 150 155 160
 Trp Arg Thr Asn Arg Asp Arg Glu Glu Ile Ser Leu Gln Glu Val Glu
 165 170 175
 Pro Val Ile Ser Arg Ala Val Met Asp Asn Pro Gln His Gly Phe Trp
 180 185 190
 Arg Ser Gly Ile Met Glu Glu His Leu Leu Asp Ala Val Val Pro Phe
 195 200 205
 Leu Pro Leu Gln Arg His His Val Arg His Cys Val Leu Asn Glu Leu
 210 215 220
 Ala Gln Leu Gly Leu Glu Pro Ala Arg Arg Trp Phe Arg Arg Cys Trp
 225 230 235 240

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<210> 13
<211> 177
<212> PRT
<213> Murine
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<220>  
<221> VARIANT  
<222> (1)...(177)  
<223> Xaa = Any Amino Acid
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[illegible]

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<210> 14
<211> 214
<212> PRT
<213> Murine
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<400> 14															
Glu	Glu	His	Pro	Leu	Val	Phe	Leu	Phe	Leu	Gly	Ser	Ser	Gly	Ile	Gly
1				5					10					15	
Lys	Thr	Glu	Leu	Ala	Lys	Gln	Thr	Ala	Lys	Tyr	Met	His	Lys	Asp	Ala
			20					25					30		
Lys	Lys	Gly	Phe	Ile	Arg	Leu	Asp	Met	Ser	Glu	Phe	Gln	Glu	Arg	His
		35					40					45			
Glu	Val	Ala	Lys	Phe	Ile	Gly	Ser	Pro	Arg	Gly	Tyr	Ile	Gly	His	Glu
	50					55					60				
Glu	Gly	Gly	Gln	Leu	Thr	Lys	Lys	Leu	Lys	Gln	Cys	Pro	Asn	Ala	Val
65					70					75					80

<210>	15
<211>	185
<212>	PRT
<213>	Unknown

<400>	15																
Pro	Gln	Gln	Pro	Thr	Gly	Ser	Phe	Leu	Phe	Leu	Gly	Pro	Thr	Gly	Val		
1				5					10					15			
Gly	Lys	Thr	Glu	Leu	Ala	Lys	Ala	Leu	Ala	Glu	Gln	Leu	Phe	Asp	Asn		
			20					25					30				
Glu	Asn	Gln	Leu	Val	Arg	Ile	Asp	Met	Ser	Glu	Tyr	Met	Glu	Gln	His		
		35					40					45					
Ser	Val	Ser	Arg	Leu	Ile	Gly	Ala	Pro	Pro	Gly	Tyr	Val	Gly	His	Glu		
	50					55					60						
Glu	Gly	Gly	Gln	Leu	Thr	Glu	Ala	Val	Arg	Arg	Arg	Pro	Tyr	Ser	Val		
65					70					75					80		
Val	Leu	Phe	Asp	Glu	Val	Glu	Lys	Ala	His	Thr	Ser	Val	Phe	Asn	Ile		
			85						90					95			
Leu	Leu	Gln	Val	Leu	Asp	Asp	Gly	Arg	Leu	Thr	Asp	Gly	Gln	Gly	Arg		
			100					105					110				
Thr	Val	Asp	Phe	Arg	Asn	Thr	Val	Ile	Ile	Met	Thr	Ser	Asn	Leu	Gly		
		115					120					125					
Ala	Glu	His	Leu	Leu	Ser	Gly	Ser	Gln	Lys	Cys	Thr	Met	Gln	Val	Ala		
	130					135					140						
Arg	Asp	Arg	Val	Met	Glu	Gln	Glu	Arg	Arg	Gln	Phe	Arg	Pro	Glu	Leu		
145				150						155				160			
Leu	Asn	Arg	Leu	Asp	Glu	Ile	Val	Val	Phe	Asp	Pro	Leu	Ser	His	Asp		
			165						170					175			
Gln	Leu	Arg	Lys	Val	Ala	Arg	Leu	Met									
			180					185									

<400> 16

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<210> 17
<211> 194
<212> PRT
<213> Homo sapien

<220>
<221> VARIANT
<222> (1)...(194)
<223> Xaa = Any Amino Acid
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<400>	17															
Pro	Lys	Lys	Pro	Leu	Thr	Leu	Ser	Leu	His	Gly	Trp	Ala	Gly	Thr	Gly	
1				5					10					15		
Lys	Asn	Phe	Val	Ser	Gln	Ile	Val	Ala	Glu	Asn	Leu	His	Pro	Lys	Gly	
			20					25					30			
Leu	Lys	Ser	Asn	Phe	Val	His	Leu	Phe	Val	Ser	Thr	Leu	His	Phe	Pro	
			35				40					45				
His	Glu	Gln	Lys	Ile	Lys	Leu	Tyr	Gln	Asp	Gln	Leu	Gln	Lys	Trp	Ile	
	50					55					60					
Arg	Gly	Asn	Val	Ser	Ala	Cys	Ala	Asn	Ser	Val	Phe	Ile	Phe	Asp	Glu	
65					70					75					80	
Met	Asp	Lys	Leu	His	Pro	Gly	Ile	Ile	Asp	Ala	Ile	Lys	Pro	Phe	Leu	
				85					90					95		
Asp	Tyr	Tyr	Glu	Gln	Val	Asp	Gly	Val	Ser	Tyr	Xaa	Lys	Ala	Ile	Phe	
			100					105					110			
Ile	Phe	Leu	Ser	Asn	Ala	Gly	Gly	Asp	Leu	Ile	Thr	Lys	Thr	Ala	Leu	
			115				120					125				
Asp	Phe	Trp	Arg	Ala	Gly	Arg	Lys	Arg	Glu	Asp	Ile	Gln	Leu	Lys	Asp	
	130					135					140					
Leu	Glu	Pro	Val	Leu	Ser	Val	Gly	Val	Phe	Asn	Asn	Lys	His	Ser	Gly	
145					150					155					160	

Leu Trp His Ser Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile
 165 170 175
 Pro Phe Leu Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala
 180 185 190
 Glu Met

<210> 18
 <211> 192
 <212> PRT
 <213> C. elegans

<400> 18
 Pro Arg Lys Pro Leu Val Leu Ser Phe His Gly Tyr Thr Gly Ser Gly
 1 5 10 15
 Lys Asn Tyr Val Ala Glu Ile Ile Ala Asn Asn Thr Phe Arg Leu Gly
 20 25 30
 Leu Arg Ser Thr Phe Val Gln His Ile Val Ala Thr Asn Asp Phe Pro
 35 40 45
 Asp Lys Asn Lys Leu Glu Glu Tyr Gln Val Glu Leu Arg Asn Arg Ile
 50 55 60
 Leu Thr Thr Val Gln Lys Cys Arg Ser Ile Phe Ile Phe Asp Glu Ala
 65 70 75 80
 Asp Lys Leu Pro Glu Gln Leu Leu Gly Ala Ile Lys Pro Phe Leu Asp
 85 90 95
 Tyr Tyr Ser Thr Ile Ser Gly Val Asp Phe Arg Arg Ser Ile Phe Ile
 100 105 110
 Leu Leu Ser Asn Lys Gly Gly Gly Glu Ile Ala Arg Ile Thr Lys Glu
 115 120 125
 Gln Tyr Glu Ser Gly Tyr Pro Arg Glu Gln Leu Arg Leu Glu Ala Phe
 130 135 140
 Glu Arg Glu Leu Met Asn Phe Ser Tyr Asn Glu Lys Gly Gly Leu Gln
 145 150 155 160
 Met Ser Glu Leu Ile Ser Asn His Leu Ile Asp His Phe Val Pro Phe
 165 170 175
 Leu Pro Leu Gln Arg Glu His Val Arg Ser Cys Val Gly Ala Tyr Leu
 180 185 190

<210> 19
 <211> 194
 <212> PRT
 <213> Homo sapien

<400> 19
 Pro Ser Lys Pro Leu Val Leu Ser Leu His Gly Trp Thr Gly Thr Gly
 1 5 10 15
 Lys Ser Tyr Val Ser Ser Leu Leu Ala Gln His Leu Phe Arg Asp Gly
 20 25 30
 Leu Arg Ser Pro His Val His His Phe Ser Pro Ile Ile His Phe Pro
 35 40 45
 His Pro Ser Arg Thr Glu Gln Tyr Lys Lys Glu Leu Lys Ser Trp Val
 50 55 60
 Gln Gly Asn Leu Thr Ala Cys Glu Arg Ser Leu Phe Leu Phe Asp Glu
 65 70 75 80
 Met Asp Lys Leu Pro Pro Gly Leu Met Glu Val Leu Gln Pro Phe Leu
 85 90 95
 Gly Pro Ser Trp Val Val Tyr Gly Thr Asn Tyr Arg Lys Ala Ile Phe
 100 105 110
 Ile Phe Ile Ser Asn Ala Gly Gly Glu Gln Ile Asn Gln Val Ala Leu
 115 120 125

Glu Ala Trp Arg Thr Asn Arg Asp Arg Glu Glu Ile Ser Leu Gln Glu
 130 135 140
 Val Glu Pro Val Ile Ser Arg Ala Val Met Asp Asn Pro Gln His Gly
 145 150 155 160
 Phe Trp Arg Ser Gly Ile Met Glu Glu His Leu Leu Asp Ala Val Val
 165 170 175
 Pro Phe Leu Pro Leu Gln Arg His His Val Arg His Cys Val Leu Asn
 180 185 190
 Glu Leu

<210> 20
 <211> 128
 <212> PRT
 <213> Murine

<220>
 <221> VARIANT
 <222> (1)...(128)
 <223> Xaa = Any Amino Acid

<400> 20
 Ala Ala Ala Leu His Gln Thr Leu Phe Ile Phe Asp Glu Ala Glu Lys
 1 5 10 15
 Leu His Pro Gly Leu Leu Glu Val Leu Gly Pro His Leu Glu Arg Arg
 20 25 30
 Ala Pro Glu Xaa Xaa Gly Leu Ser Leu Xaa Trp Thr Ile Phe Leu Phe
 35 40 45
 Leu Ser Asn Leu Arg Gly Asp Ile Ile Asn Glu Val Val Leu Lys Leu
 50 55 60
 Leu Lys Ala Gly Trp Ser Arg Glu Glu Ile Thr Met Glu His Leu Glu
 65 70 75 80
 Pro His Leu Gln Ala Glu Ile Val Asp Asp His Arg Gln Trp Leu Trp
 85 90 95
 His Ser Arg Leu Val Lys Glu Asn Leu Ile Asp Tyr Phe Ile Pro Phe
 100 105 110
 Leu Pro Leu Glu Tyr Arg His Val Arg Leu Cys Ala Arg Asp Ala Phe
 115 120 125

<210> 21
 <211> 253
 <212> DNA
 <213> Homo sapien

<400> 21
 cctggaatac aaacaccta aaatgtgtat ccgagtggaa atgcagtccc gaggctatga 60
 aattgatgaa gacattgtaa gcagagtggc tgaggagatg acatttttcc ccaaagagga 120
 gagagttttc tcagataaag gctgcaaaac ggtgttcacc aagtttagatt attactacga 180
 tgattgacag tcatgattgg cagccggagt cactgcctgg agttggaaag aaacaacact 240
 cagtccttcc acc 253

<210> 22
 <211> 253
 <212> DNA
 <213> Homo sapien

<400> 22
 ggaccttatg tttgtggatt tttacacata ggctcacctt tacgtcaggg tccgatactt 60

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taactacttc tgtaacattc gtctcaccga ctctctact gtaaaaaggg gtttctcctc 120
tctcaaaaga gtctatttcc gacgttttgc caccaagtgg ttcaatctaa taatgatgct 180
actaactgtc agtactaacc gtcggcctca gtgacggacc tcaacctttc tttgttgtga 240
gtcaggaagg tgg 253

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<210> 23
<211> 7
<212> PRT
<213> Homo sapien

```

```

<400> 23
Phe Phe Thr Met Glu Ala Val
1 5

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<210> 24
<211> 21
<212> DNA
<213> Homo sapien

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<400> 24
gtggctgaga tgacattttt c 21

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<210> 25
<211> 24
<212> DNA
<213> Homo sapien

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<400> 25
gtggctgagg agatgacatt ttcc 24

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<210> 26
<211> 8
<212> PRT
<213> Homo sapien

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<400> 26
Phe Phe Thr Met Glu Glu Ala Val
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<210> 27
<211> 205
<212> DNA
<213> Synthetic

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<400> 27
cctggaatac aaacacctaa aaatgtgtat ccgagtggaa atgcagtccc gaggctatga 60
aattgatgaa gacattgtaa gcagagtggc tgaggagatg acatttttcc ccaaagagga 120
gagagttttc tcagataaag gctgcaaaac ggtgttcacc aagtttagatt attactacga 180
tgattgacag tcattgattgg cagcc 205

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<210> 28
<211> 19
<212> DNA
<213> Synthetic

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<400> 28
cctggaatac aaacaccta 19

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<210> 29

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<211> 20
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<400> 29
 ggctgccaat catgactgtc 20

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<220>
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<400> 30
 gcaaaacagg gctttgtacc g 21

<210> 31
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<220>
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<400> 31
 agtagagacg cgggtagatg 20

<210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 32
 gcgtctctac tgccctctcg 20

<210> 33
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 33
 atgccctggc cctagttcag 20

<210> 34
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 34

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<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence
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<400> 35
gggattccaa acttccatcc
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<210> 36
<211> 20
<212> DNA
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<220>
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<400> 36
tccatgggggt tggtaggaac

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<210> 37
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<220>
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<400> 37
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<212> DNA
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<400> 38
gacccccagt agacgtttgt

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<210> 39
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<213> Artificial Sequence
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<400> 39
gtaaaaaaatc atgagccctg c

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<400> 45
ctagcacagt atgccctaag 20

<210> 46
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<400> 46
tgaggaatgt gctgagggctc 20

<210> 47
<211> 20
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<220>
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<400> 47
gctgtctcct accccatctg 20

<210> 48
<211> 283
<212> DNA
<213> Unknown

<220>
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<221> misc_feature
<222> (1)...(283)
<223> n = A,T,C or G

<400> 48
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gctgaactag gaccagggca tggagaatgg aggatggagg ccgggggatg gcaccagggc 120
cgggctagga ctagggtctg agcggggcct gggggctggg gctgggcgat ggactagggg 180
cgggttgggg ctggggctgg ggctggggga tggagcgggg ccgggggctg ggggtggggc 240
tgggggatcg actagggtct gnttaggacc aggcggttgg cat 283

<210> 49
<211> 375
<212> DNA
<213> Unknown

<220>
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<221> misc_feature
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<223> n = A,T,C or G

<400> 49
ggatggtgga tggaggctgg gggatggcag tagggccggg ctaggactgg ggctggagcg 60
gagtttgggg ctggggctca ggagcggggg ctggggctgg ggctggggct gggggatggc 120
actagggcag gccggggtag gggtcacatc ccaggagggc cgggctgggc agagctgagt 180

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ccgcgggggc cggaccccg aagccaagcn gccggcctgc aggatgagge ctggctcctc 240
ggccatgacc acagacgtgc cagacttaag tacggagacc tgaggagcca ggctgcagtt 300
ggcctacttt ncnctaagct gggggtggac cagtggtaac ctccctccga gtgggttctg 360
ctctttctag cctag                                     375

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<210> 50
<211> 439
<212> DNA
<213> Unknown

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<220>
<223> cDNA clone of DYT1 intron 1

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<221> misc_feature
<222> (1)...(439)
<223> n = A,T,C or G

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<400> 50
ccactgccac tgcaccagt ttgcaccct aaccctctgn ctgctcctcc caccccaagg 60
cagagccggn gaaaggaaac agtttggtcc ctctgggtcg gctgcggaag agtctcacca 120
tcctttctgt tccgtagcta gaaaggaggc agaaccaca ttcggaggga ggttaccact 180
ggtccacccc cagcttagcg caaagtaggc caacctgcat gcctggnnct cctcaggntc 240
tgctacttta agtctggcag ctctnnmtca tggccgaggt agccaggctc atcctgcagg 300
nncengcenn ttgncttncc ggggtntcgn nccccgtac tcagctcgtc cagccggcct 360
ctggatgtga cctaccgctg ctagtgcac ccagccagcc agccagccgt ctagccagcc 420
aactgctcag ccagtctag                                     439

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<210> 51
<211> 368
<212> DNA
<213> Unknown

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<220>
<223> cDNA clone of DYT1 intron 1

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<221> misc_feature
<222> (1)...(368)
<223> n = A,T,C or G

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<400> 51
caaagccaat caggagtggg gaagaaacac ggcaaaatgt agccacattt acagcccata 60
aganagccag caaagccgtc tagcctccaa gcaccttgcg aaacctcaag tactgcggtc 120
tggtaaagct ctggcccaga ggggacggcg gtccaggng cctcccttt gctggtcctg 180
cctattctaa agccctggcc cgntccttc ccgaaaagcc ccttggtgcc actgccactg 240
ccaccanttt gnccccctac ccctgtntcg ctctccccc cccaaggcag atgcggnnng 300
ngaaaggaaa cantttggtc cctcctggtc ggctcgngga agactcctca ccaccttcc 360
tgtcttcc                                     368

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<210> 52
<211> 400
<212> DNA
<213> Unknown

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<220>
<223> cDNA clone of DYT1 intron 2

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<400> 52
gaatatttac gaggtgtgtc tgaacagtga ctatgtccac ctgtttgtgg ccacattgct 60
ctttccacat gcttcaaaca tcaccttgta caaggcaagg atggaagttt ggaatccctt 120
cctggatgtc atcgggtttg ggggtctctt gttgtgggat gagatttggg agttctatgt 180

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tgaaatgagt gagcccgga aacggttcat gtctcagttc cccttggaaa ggtgtagaag 240
ttaagagttt gagatgctgt gagcagttaa taccatcaaa gctttgtggt gggttctgaa 300
aatcgggtcca gtgagtatgt agggtcattg gatttttagag gtggacatga tcaaattccat 360
cttagagatc aacacatctc actcattttt attttcttat 400

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<210> 53
<211> 418
<212> DNA
<213> Unknown

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<220>
<223> cDNA clone of DYT1 intron 2

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<221> misc_feature
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<223> n = A,T,C or G

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<400> 53
tttggagtga gacaggactg ggttcaggtc ccagctctgc cacatatagt cttgggcaag 60
tggaagtaagc gctctctgtg cctcagttcc ctcatctgta aaatgagaac gatagtggcc 120
actccatggg gttggttagga acaaagaaga ttttgggcat gtaaagtct tagtgccgag 180
tgcacagtgg tctgtaagtg aagctgcggg tcttagtggt agaaggagct gattgatggc 240
cctggctgag aactttgtgt tcgctttttc ccnttttaac tcaggatcag ttacagttgt 300
ggattcgagg caacgtgagt gcctgtgcga ggtccatctt catatttgat gaaatggata 360
agatgcatgc aggccatcata gatgccttca ancctttcct cgactattat gacctggt 418

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<210> 54
<211> 198
<212> DNA
<213> Unknown

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<220>
<223> cDNA clone of DYT1 intron 3

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<400> 54
ctcgactatt atgacctggt ggatgggggc tcctaccaga aagccatggt catattttctc 60
aggtaaagtc agggctagga catgatggat gggccccgag cccaagcctc tgagctccag 120
gagaaaaccc tgccttacc cactgggatt gttttgcagc aatgctggag cagaaaggat 180
cacagatgtg tttggatt 198

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<210> 55
<211> 536
<212> DNA
<213> Unknown

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<220>
<223> cDNA clone of DYT1 intron 4

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<221> misc_feature
<222> (1)...(536)
<223> n = A,T,C or G

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<400> 55
gtctgtgtcg gttttcaata acaagaacag gtgagttagg ccatccaccg ccagtcccat 60
ctggttccta atcctgcacc ctaagtgtta aaagcatcag ggtcactgtc agcatcacct 120
gggagctggg tagaaagaaa tggagattct cagtccccct ccgagtcatt aggggaattc 180
ttgctgatga actccaggta acttttatga acactaatgt ttgacaagtg ctgtttttatt 240
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ctcactgcaa cctctgcctc ccgggctcaa gcgattcttg tgctcagcc tcctgagtag 360
ctgggattac aggtgcacac catgcccacg cnaatatatt gtatttttag tagaganggg 420

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gccccgtncatggttaaccag gctgggtcttg aactnttacc tcagggtgagt ccnccacctc 480
 ggcctcccaa agtgctggga ttacaggcgt gagccactgt gtctcagctt attttt 536

<210> 56
 <211> 1302
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 4

<221> misc_feature
 <222> (1)...(1302)
 <223> n= A,T,C or G; m= A,or C; r= G,or A; w= A,or T; y= C,or T

<400> 56
 gccactccaa gctaccatct gagattgttt cctgccctag agtggttaaag gcgtgaggtc 60
 cgtctgccct cagctgtgtc cccaggccca gggcgtgcct ggcaacanna gcaggcctct 120
 gagaaccagc ctcccacgtg agttcatgat agnaagacag cccctcgttc ccattcagtg 180
 gtttggttctg ttcttttycct ggcmataaag tccactctgy mrtcagccam acatttattg 240
 agtaccagtt gttggcaaag cactgtttggg catgaaaagc attaacccag tgaatgagga 300
 ggagcttggg ttgggacgga gccmcaraaw tacatggcag accagaagga aatcagctca 360
 agtagaaaara cacgcatggg ctctgtgggag acgcagtgtg tgctgtgtca tctggggctg 420
 ggaggaagtg tcttgatca ggagttccag gagccagga ggagtggacg ggtcagtga 480
 gagccagccc gcaatcaggg gaagaaaaca cggccaaggc caggccttca cggggagccc 540
 agcgtgggct gcacatctgc actctccagg ctagttttgg tgcccacatg ctctgcaggg 600
 tctgggcact gtggcagcgg cagcaggcct ccctgttgct agtccagctg ctgaaactcc 660
 agggagagtc aaaaagttcc caaatacaga ggcgtggctg gtagtccttc ccgggaattc 720
 ttcttgcttc ccgctttctg tggaaactctg ccttccccac tctgcctctc tgcttgttcc 780
 tgggccccag gacctcttcc ccatcttcca tctcttaagt cataccttgg gaggcctccc 840
 ccagcccgcc gtgtaaagag ggctgtcaca gcttctgctg tcacagaagc attacaatgt 900
 gcaggtgcct gttaacatct gccttccccca ctgatctgga gctccacaag ggagagggca 960
 caccagtag gtatgtgtgg gatggatagg aggggtggatg acaccagta gatgtgtatg 1020
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 ggaggcgtct atagggcagg tgggtggatg tggatgaaca gcacctgtt tcttcttccc 1260
 aggtggcttc tggcacagca gcttaattga ccggaacctc at 1302

<210> 57
 <211> 240
 <212> DNA
 <213> Unknown

<220>
 <223> TORB intron 1-5'

<221> misc_feature
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 <223> n = A,T,C or G

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 cccgtggcat ctagacggcg gtggtcccag ctggggtggg cggggagcgg atggggcggc 180
 cccggaaccg ttcgcnggaa cgcagaagcn gtgccttgaa acactctcag atcgtgnggc 240

<210> 58
 <211> 310

<212> DNA
<213> Unknown

<220>
<223> TORB intron 1-3'

<221> misc_feature
<222> (1)...(310)
<223> n = A,T,C or G

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gggaccaaag gacgtccgtc gttcccacccg accctaatacg ttcgcgngtc ngttcgctac 60
ccagtagaga gacttactta cnngtnnatc gaaggaatag tctggggcctt cgcaattcct 120
ggaggtgtat tagaactttc accgtagcaa actgacggag ccgggatccc acaccgcctg 180
tgggnncgac acgggaccta ttgacacgaa gaacgaaacn gtcgattctt tcacgacgca 240
acgactacgt aaaaattcca gacaaagaga gaaacaagac cccgacaaga acgtcgagag 300
ttcgacctaa                                     310
```

<210> 59
<211> 401
<212> DNA
<213> Unknown

<220>
<223> TORB intron 2-5'

<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

```
<400> 59
caggaacaac aaaaatccca agaaaccact gaccctttcc ttacacggct gggctggcac 60
aggcaagaat tttgtcagtn aaattgtggc tgaaaatctt cacccaaaag gtctgaagag 120
taactttgtc cacctgtttg tategactct gcaattccct catgagcaga agataaaaact 180
gtaccaggca agagaacccg ctattatctc gtctgcaggc cagtcggact ggtccgggtg 240
acctgtcac taactctggc ctctgcttct ctttcctttg tgttgctgta gcccccgct 300
ccactgagtt aaggcacact tagtccaggt agttacaaag ctctctaca acatttctta 360
cttggttcca aaacagtcca gtggggtagg ggatgttatt t                                     401
```

<210> 60
<211> 238
<212> DNA
<213> Unknown

<220>
<223> TORB intron 2-3'

```
<400> 60
ttctgtaact ggtcctggac caaccatgaa agaagaaaca ggatgcgaag ctcaaagggc 60
tgcaccaaga ggcgcgcagg ctccatctgc tctcatgca ctgaaggacg aggtcagagc 120
tcttagaatg gcaccctcac cccactcgc taggtagcag cttttctaaa accttatctc 180
taaaaagtgg aaattggcag agatagatgc taaaatgcag agaagttttt cctaactc 238
```

<210> 61
<211> 391
<212> DNA
<213> Unknown

<220>
<223> TORB intron 3-5'

<220>

<223> Synthetic Oligonucleotide

<400> 64
gaattcctta ag

12

<210> 65
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<223> Xaa at position 2, 5 is a variable residue
Xaa at position 8 is a threonine or a serine
residue

<221> VARIANT
<222> (1)...(8)
<223> Xaa = Any Amino Acid

<400> 65
Gly Xaa Thr Gly Xaa Gly Lys Xaa
1 5

<210> 66
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<223> Xaa at position 2, 3, 4, 8 is a hydrophobic residue
Xaa at position 11 is a variable residue

<221> VARIANT
<222> (1)...(12)
<223> Xaa = Any Amino Acid

<400> 66
Ser Xaa Xaa Xaa Phe Asp Glu Xaa Glu Lys Xaa His
1 5 10

<210> 67
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of DYT1

<400> 67
gtaggctggg

10

<210> 68
<211> 10
<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 68
gcaaggatgg

10

<210> 69
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 69
gtaaggtcag

10

<210> 70
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 70
gtgagtaggg

10

<210> 71
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 71
tctttcccag

10

<210> 72
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 72
tttaattcag

10

<210> 73
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 73
tgttttgcag 10

<210> 74
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of DYT1

<400> 74
ttcttcccag 10

<210> 75
<211> 11
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of DYT1

<400> 75
cactgcagaa g 11

<210> 76
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of DYT1

<400> 76
caatgctgga 10

<210> 77
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 77
tggcttctgg 10

<210> 78
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 78
gcaagagaac 10

<210> 79
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 79
gtcagcggga 10

<210> 80
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 80
gtgagtccac 10

<210> 81
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 81
gttcttgacag 10

<210> 82
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 82
gttgggtccag 10

<210> 83
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 83
gcaaactcag 10

<210> 84
<211> 9

<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 84
tggtctgag 9

<210> 85
<211> 11
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 85
ctctcaagct g 11

<210> 86
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 86
caatgcaggc 10

<210> 87
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 87
tggcctgtgg 10

<210> 88
<211> 378
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 1

<221> misc_feature
<222> (1)...(378)
<223> n = A,T,C or G

<400> 88
ctgggaaaga caaagccaat caggagtggg gaagaaacac ggcaaaatgt agccacattt 60
acagcccata aganagccag caaagccgctc tagcctccaa gcaccttgcg aaacctcaag 120
tactgcggtc tggtaagctc ctggcccaga ggggacggcg gtccaggng cctcccttt 180
gctggtcctg cctattctaa agcctggcc cgnctccttc ccgaaaagcc ccttggtgcc 240

```

actgccactg ccaccanttt gcncccctac cctgtgntctg ctctctccac cccaaggcag 300
atgcggnngg ngaaaggaaa cantttggtc cctctgggtc ggctcgngga agactcctca 360
ccatccttcc tgtcttcc                                     378

```

```

<210> 89
<211> 402
<212> DNA
<213> Unknown

```

```

<220>
<223> cDNA clone of DYT1 intron 2

```

```

<400> 89
gaatatttac gagggtggtc tgaacagtga ctatgtccac ctgtttgtgg ccacattgct 60
ctttccacat gcttcaaaca tcaccttgta caaggcaagg atggaagttt ggaatccctt 120
cctggatgtc atcgggtttg ggggtctctt gttgtgggat gagatttggg agttctatgt 180
tgaaatgagt gagcccgaa aacggttcat gtctcagttc cccttggaaa ggtgtagaag 240
ttaagagttt gagatgcgtg gagcagttaa taccatcaa gctttgtggt gggttctgaa 300
aatcggtcca gtgagtatgt agggtcattg gatttttagag gtggacatga tcaaattccat 360
cttagagatc aacacatctc actcattttt attttcttat tt                                     402

```

```

<210> 90
<211> 200
<212> DNA
<213> Unknown

```

```

<220>
<223> cDNA clone of DYT1 intron 3

```

```

<400> 90
ctcgactatt atgacctggt ggatggggtc tcctaccaga aagccatggt catattttctc 60
aggtaagggtc agggctagga catgatggat gggccccgag cccaagcctc tgagctccag 120
gagaaaaccc tgccttacc cactgggatt gttttgcagc aatgctggag cagaaaggat 180
cacagatgtg gctttggatt                                     200

```